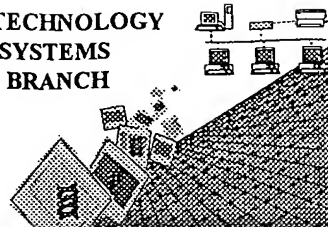


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/069,228A  
Source: PO/10  
Date Processed by STIC: 10/30/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
**VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 19/069,228A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences  
(OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 1-20, 22-23 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT

## RAW SEQUENCE LISTING

DATE: 10/30/2002

PATENT APPLICATION: US/10/069,228A

TIME: 16:02:40

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\10302002\J069228A.raw

3 <110> APPLICANT: Takeda Chemical Industries, Ltd.  
 W--> 4 <120> TITLE OF INVENTION: Screening Method  
 W--> 5 <130> FILE REFERENCE: 2639WOOP  
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/069,228A  
 C--> 6 <141> CURRENT FILING DATE: 2002-07-22  
 6 <150> PRIOR APPLICATION NUMBER: JP 11-236597  
 7 <151> PRIOR FILING DATE: 1999-08-24  
 W--> 8 <160> NUMBER OF SEQ ID: 23

## ERRORED SEQUENCES

63 <210> SEQ ID NO: 7  
 64 <211> LENGTH: 7  
 65 <212> TYPE: PRT  
 66 <213> ORGANISM: Artificial Sequence  
 67 <220> FEATURE:  
 68 <223> OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form  
 E--> 69 <233> Xaa means pGlu  
 W--> 70 <400> SEQUENCE: 7  
 W--> 71 Xaa Asp Pro Phe Leu Arg Phe  
 72 1 5  
 228 <210> SEQ ID NO: 23  
 229 <211> LENGTH: 30  
 230 <212> TYPE: DNA  
 231 <213> ORGANISM: Artificial Sequence  
 W--> 232 <220> FEATURE:  
 233 <223> OTHER INFORMATION: see item 11 on Erra Summary Sheet  
 W--> 234 <400> SEQUENCE: 23  
 C--> 235 gctagctcag gatggatcgg tctcttgctg 30  
 E--> 239  
 ① delete

Does Not Comply  
 Corrected Diskette Needed

While valid,  
 FYI: This response does not explain

the  
 source  
 of genetic  
 material  
 for Artificial  
 Sequence

(see item 11  
 on Erra  
 Summary  
 Sheet)

This is  
 a global  
 error.

1) Please consult Sequence Rules  
 for valid format.

2) Per 1.822 of Sequence Rules, number the  
 amino acids under every 5 amino acids

3) All nucleotides MUST be in lower-case letters,

## VARIABLE LOCATION SUMMARY

DATE: 10/30/2002

PATENT APPLICATION: US/10/069,228A

TIME: 16:02:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\10302002\J069228A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:7; Xaa Pos. 1

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/069,228A

DATE: 10/30/2002  
TIME: 16:02:41

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF4\10302002\J069228A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:270 C: Current Application Number differs, Replaced Current Application No  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:8 M:283 W: Missing Blank Line separator, <160> field identifier  
L:9 M:283 W: Missing Blank Line separator, <210> field identifier  
L:13 M:283 W: Missing Blank Line separator, <220> field identifier  
L:15 M:283 W: Missing Blank Line separator, <400> field identifier  
L:22 M:283 W: Missing Blank Line separator, <220> field identifier  
L:24 M:283 W: Missing Blank Line separator, <400> field identifier  
L:31 M:283 W: Missing Blank Line separator, <220> field identifier  
L:33 M:283 W: Missing Blank Line separator, <400> field identifier  
L:40 M:283 W: Missing Blank Line separator, <220> field identifier  
L:42 M:283 W: Missing Blank Line separator, <400> field identifier  
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:41  
L:49 M:283 W: Missing Blank Line separator, <220> field identifier  
L:51 M:283 W: Missing Blank Line separator, <400> field identifier  
L:58 M:283 W: Missing Blank Line separator, <220> field identifier  
L:60 M:283 W: Missing Blank Line separator, <400> field identifier  
L:67 M:283 W: Missing Blank Line separator, <220> field identifier  
L:69 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:70 M:283 W: Missing Blank Line separator, <400> field identifier  
L:71 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7  
L:71 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7  
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
L:77 M:283 W: Missing Blank Line separator, <220> field identifier  
L:79 M:283 W: Missing Blank Line separator, <400> field identifier  
L:86 M:283 W: Missing Blank Line separator, <220> field identifier  
L:88 M:283 W: Missing Blank Line separator, <400> field identifier  
L:95 M:283 W: Missing Blank Line separator, <220> field identifier  
L:97 M:283 W: Missing Blank Line separator, <400> field identifier  
L:104 M:283 W: Missing Blank Line separator, <220> field identifier  
L:106 M:283 W: Missing Blank Line separator, <400> field identifier  
L:113 M:283 W: Missing Blank Line separator, <220> field identifier  
L:115 M:283 W: Missing Blank Line separator, <400> field identifier  
L:122 M:283 W: Missing Blank Line separator, <220> field identifier  
L:124 M:283 W: Missing Blank Line separator, <400> field identifier  
L:131 M:283 W: Missing Blank Line separator, <220> field identifier  
L:133 M:283 W: Missing Blank Line separator, <400> field identifier  
L:140 M:283 W: Missing Blank Line separator, <220> field identifier  
L:142 M:283 W: Missing Blank Line separator, <400> field identifier  
L:151 M:283 W: Missing Blank Line separator, <220> field identifier  
L:153 M:283 W: Missing Blank Line separator, <400> field identifier  
L:162 M:283 W: Missing Blank Line separator, <220> field identifier  
L:164 M:283 W: Missing Blank Line separator, <400> field identifier  
L:171 M:283 W: Missing Blank Line separator, <220> field identifier  
L:173 M:283 W: Missing Blank Line separator, <400> field identifier  
L:180 M:283 W: Missing Blank Line separator, <220> field identifier

## VERIFICATION SUMMARY

DATE: 10/30/2002

PATENT APPLICATION: US/10/069,228A

TIME: 16:02:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\10302002\J069228A.raw

L:182 M:283 W: Missing Blank Line separator, <400> field identifier  
L:189 M:283 W: Missing Blank Line separator, <220> field identifier  
L:191 M:283 W: Missing Blank Line separator, <400> field identifier  
L:198 M:283 W: Missing Blank Line separator, <400> field identifier  
L:199 M:112 C: (48) String data converted to lower case,  
M:112 Repeated in SeqNo=21  
L:224 M:283 W: Missing Blank Line separator, <220> field identifier  
L:226 M:283 W: Missing Blank Line separator, <400> field identifier  
L:226 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:225  
L:227 M:112 C: (48) String data converted to lower case,  
L:232 M:283 W: Missing Blank Line separator, <220> field identifier  
L:234 M:283 W: Missing Blank Line separator, <400> field identifier  
L:234 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:233  
L:235 M:112 C: (48) String data converted to lower case,  
L:239 M:254 E: No. of Bases conflict, this line has no nucleotides.